

10/526650

1/14

DT01 Rec'd PCT/PTC 03 MAR 2005

SEQUENCE LISTING

<110> DNAVEC RESEARCH INC.

<120> Methods of producing a viral vector comprising a membrane protein
that binds to sialic acid as a component of the envelope
using neuraminidase derived from Gram-positive bacteria

<130> D3-A0204P

<150> JP 2002-258576

<151> 2002-09-04

<160> 2

<170> PatentIn version 3.1

<210> 1

<211> 1941

<212> DNA

<213> Micromonospora viridifaciens

<220>

<221> CDS

<222> (1)..(1941)

<223>

<400> 1

atg act gcg aat ccg tac ctc cgc cgc ctg ccc cgg cgc cga gcc gtc 48

Met Thr Ala Asn Pro Tyr Leu Arg Arg Leu Pro Arg Arg Arg Ala Val

1 5 10 15

agc ttc ctg ctc gca cca gcg ctg gcg gcc gcc acg gtc gcc ggc gcg 96

Ser Phe Leu Leu Ala Pro Ala Leu Ala Ala Ala Thr Val Ala Gly Ala

20 25 30

tcc ccc gca cag gcc atc gcc ggg gca ccc gtc ccg ccc ggc ggc gag 144

Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu

35 40 45

ccg ctc tac acg gag cag gac ctc gcc gtg aac ggc agg gag ggc ttt 192

Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe

50 55 60

ccg aac tac cgc atc cca gcg ctg acc gtc acg ccc gac ggg gac ctg 240

Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu

65 70 75 80

ctg gcc tcg tac gac ggc cgc ccg acc ggt atc gac gcg ccc ggc ccc 288

Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro

85 90 95

aac tcc atc ctc caa cgc cgc agc acc gac ggc ggc cg ^g acg tgg ggc	336		
Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly			
100	105	110	
gag caa cag gtc gtc agc gcc ggc cag acc acc gc ^g cc ^g atc aag ggg	384		
Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly			
115	120	125	
ttc tcc gac ccc agc tac ctt gtc gac cg ^g gaa acc ggg acc atc ttc	432		
Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe			
130	135	140	
aac ttc cac gtc tac tcc cag cg ^g cag ggc ttc gcc ggc agc cg ^g ccc	480		
Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro			
145	150	155	160
ggc acc gac cg ^g gca gac ccc aac gtg ctc cac gcc aac gtc gc ^g acc	528		
Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr			
165	170	175	
tcg acc gac ggc ggt ctg acc tgg tcg cac cg ^g acc atc acg gcc gac	576		
Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp			
180	185	190	
atc acc ccg gat ccg ggc tgg cgc agc cg ^g ttc gcc gcc tcc ggc gaa	624		
Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu			

195	200	205	
<pre>ggc atc cag ctc cgc tat gga ccc cac gcc ggt cga ctc atc cag cag 672 Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln</pre>			
210	215	220	
<pre>tac acg atc atc aac gct gcc ggc gcc ttc cag gcg gtg agc gtg tac 720 Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr</pre>			
225	230	235	240
<pre>agc gac gac cac gga agg acc tgg cgc gcc ggc gaa gcc gtc ggg gtc 768 Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val</pre>			
245	250		255
<pre>ggc atg gac gag aac aag acc gtc gaa ctc tcc gat ggc cgg gtc ctg 816 Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu</pre>			
260	265		270
<pre>ctc aac agc cgc gac tcg gcc cgc agc gga tac cgt aag gtg gcc gtc 864 Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val</pre>			
275	280		285
<pre>tcc act gac ggc ggc cac agc tac ggc ccg gtg acc atc gac cgc gac 912 Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp</pre>			
290	295		300

ctc ccc gac ccg acg aac aac gca tcg atc atc cgg gcc ttc cct gac			960
Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp			
305	310	315	320
gcc ccg gcc ggc tcc gcg cgg gcc aag gtc ctg ctc ttc tcc aac gcc			1008
Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala			
325	330	335	
gcc agc cag acc tcg cgc agt cag ggc acc atc cgg atg tcc tgc gac			1056
Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp			
340	345	350	
gat ggc cag acc tgg ccg gtt tcg aag gtc ttc cag ccc ggc tcg atg			1104
Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met			
355	360	365	
tcg tac tcc acc ctg acc gca ctg ccc gac ggc acc tac ggg ctg ctg			1152
Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu			
370	375	380	
tac gag ccg ggc acc ggc atc aga tac gcc aac ttc aac ctc gcc tgg			1200
Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp			
385	390	395	400
ctg ggc ggc atc tgc gcg ccc ttc acg att ccg gat gtg gcg ctc gag			1248
Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu			

405	410	415	
			1296
ccg ggc cag cag gtc act gtt ccg gtg gcc gtc acg aac cag tcc ggt Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly			
420	425	430	
			1344
atc gcg gta ccg aag ccg agc ctt cag ctc gac gca tcg ccg gac tgg Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp			
435	440	445	
			1392
cag gtt cag ggt tcc gtc gag ccc ctc atg ccc gga cgg cag gcc aag Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys			
450	455	460	
			1440
ggc cag gtg acc atc acg gtt ccc gcc ggc acc acc ccc ggt cgc tac Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr			
465	470	475	480
			1488
cgg gtc ggt gcg acg ctg cgc acc tcc gcg ggt aac gcg tcg acg acc Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr			
485	490	495	
			1536
ttc acg gtc acg gtt gga ctg ctc gac cag gcc cggt atg agc atc gcg Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala			
500	505	510	

gac gtc gac agc gag gag acc gcc cgc gaa gac ggg cgg gcg agc aac			1584
Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn			
515	520	525	
gtg atc gac ggc aac ccc tcg acg ttc tgg cac acc gaa tgg tcg cgt			1632
Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg			
530	535	540	
gcc gat gct cct ggc tac ccg cac cgc atc agc ctc gac ctc ggt ggc			1680
Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly			
545	550	555	560
acg cac acg atc agc ggc ctc cag tac acc cga cgg cag aac agc gcc			1728
Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala			
565	570	575	
aac gag cag gtc gcg gac tac gag atc tac acc agc ctg aac ggc acg			1776
Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr			
580	585	590	
acc tgg gat ggc ccg gtt gcc agc ggg cgc ttc acc acg tcc ctc gcg			1824
Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala			
595	600	605	
ccg cag cgc gcg gtc ttc ccg gcg cgg gac gcc agg tac atc cgg ttg			1872
Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu			

610

615

620

gtg gcc ctc agc gag cag acc ggg cac aag tac gcc gcg gtc gct gag 1920
Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu

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630

635

640

ctg gag gtg gaa ggc cag cgc 1941
Leu Glu Val Glu Gly Gln Arg

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<210> 2

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<212> PRT

<213> Micromonospora viridifaciens

<400> 2

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20 25 30

Ser Pro Ala Gln Ala Ile Ala Gly Ala Pro Val Pro Pro Gly Gly Glu

35

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45

Pro Leu Tyr Thr Glu Gln Asp Leu Ala Val Asn Gly Arg Glu Gly Phe

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60

Pro Asn Tyr Arg Ile Pro Ala Leu Thr Val Thr Pro Asp Gly Asp Leu

65

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75

80

Leu Ala Ser Tyr Asp Gly Arg Pro Thr Gly Ile Asp Ala Pro Gly Pro

85

90

95

Asn Ser Ile Leu Gln Arg Arg Ser Thr Asp Gly Gly Arg Thr Trp Gly

100

105

110

Glu Gln Gln Val Val Ser Ala Gly Gln Thr Thr Ala Pro Ile Lys Gly

115

120

125

Phe Ser Asp Pro Ser Tyr Leu Val Asp Arg Glu Thr Gly Thr Ile Phe

130

135

140

Asn Phe His Val Tyr Ser Gln Arg Gln Gly Phe Ala Gly Ser Arg Pro

145 150 155 160

Gly Thr Asp Pro Ala Asp Pro Asn Val Leu His Ala Asn Val Ala Thr

165 170 175

Ser Thr Asp Gly Gly Leu Thr Trp Ser His Arg Thr Ile Thr Ala Asp

180 185 190

Ile Thr Pro Asp Pro Gly Trp Arg Ser Arg Phe Ala Ala Ser Gly Glu

195 200 205

Gly Ile Gln Leu Arg Tyr Gly Pro His Ala Gly Arg Leu Ile Gln Gln

210 215 220

Tyr Thr Ile Ile Asn Ala Ala Gly Ala Phe Gln Ala Val Ser Val Tyr

225 230 235 240

Ser Asp Asp His Gly Arg Thr Trp Arg Ala Gly Glu Ala Val Gly Val

245

250

255

Gly Met Asp Glu Asn Lys Thr Val Glu Leu Ser Asp Gly Arg Val Leu

260

265

270

Leu Asn Ser Arg Asp Ser Ala Arg Ser Gly Tyr Arg Lys Val Ala Val

275

280

285

Ser Thr Asp Gly Gly His Ser Tyr Gly Pro Val Thr Ile Asp Arg Asp

290

295

300

Leu Pro Asp Pro Thr Asn Asn Ala Ser Ile Ile Arg Ala Phe Pro Asp

305

310

315

320

Ala Pro Ala Gly Ser Ala Arg Ala Lys Val Leu Leu Phe Ser Asn Ala

325

330

335

Ala Ser Gln Thr Ser Arg Ser Gln Gly Thr Ile Arg Met Ser Cys Asp

340

345

350

Asp Gly Gln Thr Trp Pro Val Ser Lys Val Phe Gln Pro Gly Ser Met

355

360

365

Ser Tyr Ser Thr Leu Thr Ala Leu Pro Asp Gly Thr Tyr Gly Leu Leu

370

375

380

Tyr Glu Pro Gly Thr Gly Ile Arg Tyr Ala Asn Phe Asn Leu Ala Trp

385

390

395

400

Leu Gly Gly Ile Cys Ala Pro Phe Thr Ile Pro Asp Val Ala Leu Glu

405

410

415

Pro Gly Gln Gln Val Thr Val Pro Val Ala Val Thr Asn Gln Ser Gly

420

425

430

Ile Ala Val Pro Lys Pro Ser Leu Gln Leu Asp Ala Ser Pro Asp Trp

435

440

445

Gln Val Gln Gly Ser Val Glu Pro Leu Met Pro Gly Arg Gln Ala Lys
450 455 460

Gly Gln Val Thr Ile Thr Val Pro Ala Gly Thr Thr Pro Gly Arg Tyr
465 470 475 480

Arg Val Gly Ala Thr Leu Arg Thr Ser Ala Gly Asn Ala Ser Thr Thr
485 490 495

Phe Thr Val Thr Val Gly Leu Leu Asp Gln Ala Arg Met Ser Ile Ala
500 505 510

Asp Val Asp Ser Glu Glu Thr Ala Arg Glu Asp Gly Arg Ala Ser Asn
515 520 525

Val Ile Asp Gly Asn Pro Ser Thr Phe Trp His Thr Glu Trp Ser Arg
530 535 540

Ala Asp Ala Pro Gly Tyr Pro His Arg Ile Ser Leu Asp Leu Gly Gly
545 550 555 560

Thr His Thr Ile Ser Gly Leu Gln Tyr Thr Arg Arg Gln Asn Ser Ala

565 570 575

Asn Glu Gln Val Ala Asp Tyr Glu Ile Tyr Thr Ser Leu Asn Gly Thr

580 585 590

Thr Trp Asp Gly Pro Val Ala Ser Gly Arg Phe Thr Thr Ser Leu Ala

595 600 605

Pro Gln Arg Ala Val Phe Pro Ala Arg Asp Ala Arg Tyr Ile Arg Leu

610 615 620

Val Ala Leu Ser Glu Gln Thr Gly His Lys Tyr Ala Ala Val Ala Glu

625 630 635 640

Leu Glu Val Glu Gly Gln Arg

645